

TECH CENTER 1600/2900

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1 SEQUENCE LISTING

<110> Buechler, Valkirs, Gunars Gray, Jeff Lonberg, Nils Biosite Diagnostics, Inc. GenPharm International

<120> Human Antibodies

<130> 020015-000110US

<140> 09/453,234 <141> 1999-12-01

<150> US 60/157,415 <151> 1999-10-02

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Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu

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65

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11

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•																
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•																
tat Tyr	gat Asp 50	gca Ala	tcc Ser	aac Asn	agg Arg	gcc Ala 55	Thr	ggc	ato Ile	cca Pro	gcc Ala 60	Arg	tto Phe	agt Ser	ggc	192
agt Ser 65	gly aaa	tct Ser	Gly 999	aca Thr	gac Asp 70	Phe	act Thr	ctc Leu	acc Thr	ato Ile 75	Ser	agc Ser	cta Leu	gag Glu	g cct Pro 80	240
gaa Glu	gat Asp	ttt Phe	gca Ala	gtt Val 85	Tyr	tac Tyr	tgt Cys	cag Gln	cag Gln 90	Arg	agc Ser	aac Asn	tgg Trp	cct Pro 95	ccc Pro	288
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cca Pro	tct Ser	gtc Val 115	ttc Phe	atc Ile	ttc Phe	ccg Pro	cca Pro 120	tct Ser	gat Asp	gag Glu	cag Gln	ttg Leu 125	aaa Lys	tct Ser	gga Gly	384
act Thr	gcc Ala 130	tct Ser	gtt Val	gtg Val	tgc Cys	ctg Leu 135	ctg Leu	aat Asn	aac Asn	ttc Phe	tat Tyr 140	ccc Pro	aga Arg	gag Glu	gcc Ala	432
aaa Lys 145	gta Val	cag Gln	tgg Trp	aag Lys	gtg Val 150	gat Asp	aac Asn	gcc Ala	ctc Leu	caa Gln 155	tcg Ser	ggt Gly	aac Asn	tcc Ser	cag Gln 160	480
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agc Ser	acc Thr	ctg Leu	acg Thr 180	ctg Leu	agc Ser	aaa Lys	gca Ala	gac Asp 185	tac Tyr	gag Glu	aaa Lys	cac His	aaa Lys 190	gtc Val	tac Tyr	576
gcc Ala	Cys	gaa Glu 195	gtc Val	acc Thr	cat His	cag Gln	ggc Gly 200	ctg Leu	agc Ser	tcg Ser	ccc Pro	gtc Val 205	aca Thr	aag Lys	agc Ser	624
Phe	aac Asn 210	agg Arg	gga Gly	gag Glu	tct Ser	tat Tyr 215	cca Pro	tat Tyr	gat Asp ·	gtg Val	cca Pro 220	gat Asp	tat Tyr	gcg Ala	agc Ser	672
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Lou	71 - r	r r	Ta	C1 ~	01 -	T	D	~ 1	~ 1		_	_	_	_		

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile 35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala 105 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly 120 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala 135 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln 150 155 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser 165 170 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr 185 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser 200 Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser 215 <210> 47 <211> 672 <212> DNA <213> Homo sapiens <220> <223> M1-21L <220> <221> CDS <222> (1)..(672) <400> 47 gcc atc cgg atg acc cag tct cca tcc ttc ctg tct gca tct gta gga Ala Ile Arg Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly gac aga gtc acc atc act tgc cgg gca agt cag agc att agc agc tat Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr 20 tta aat tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile 35

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agt Ser 65	gga Gly	tct Ser	Gly aaa	aca Thr	gat Asp 70	ctc Leu	act Thr	ctc Leu	acc Thr	atc Ile 75	agc Ser	agt Ser	ctg Leu	caa Gln	cct Pro 80	240
gaa Glu	gat Asp	ttt Phe	gca Ala	act Thr 85	tat Tyr	tac Tyr	tgt Cys	cag Gln	tgt Cys 90	ggt Gly	tac Tyr	agt Ser	aca Thr	cca Pro 95	ttc Phe	288
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cca Pro	tct Ser	gtc Val 115	ttc Phe	atc Ile	ttc Phe	ccg Pro	cca Pro 120	tct Ser	gat Asp	gag Glu	cag Gln	ttg Leu 125	aaa Lys	tct Ser	gga Gly	384
act T <u>h</u> r	gcc Ala 130	tct Ser	gtt Val	gtg Val	tgc Cys	ctg Leu 135	ctg Leu	aat Asn	aac Asn	ttc Phe	tat Tyr 140	ccc Pro	aga Arg	gag Glu	gcc Ala	432
aaa Lys 145	gta Val	cag Gln	tgg Trp	aag Lys	gtg Val 150	gat Asp	aac Asn	gcc Ala	ctc Leu	caa Gln 155	tcg Ser	ggt Gly	aac Asn	tcc Ser	cag Gln 160	480
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agc Ser	acc Thr	ctg Leu	acg Thr 180	ctg Leu	agc Ser	aaa Lys	gca Ala	gac Asp 185	tac Tyr	gag Glu	aaa Lys	cac His	aaa Lys 190	gtc Val	tac Tyr	576
gcc Ala	tgc Cys	gaa Glu 195	gtc Val	acc Thr	cat His	cag Gln	ggc Gly 200	ctg Leu	agc Ser	tcg Ser	ccc Pro	gtc Val 205	aca Thr	aag Lys	agc Ser	624
ttc Phe	aac Asn 210	agg Arg	gga Gly	gag Glu	tct Ser	tat Tyr 215	cca Pro	tat Tyr	gat Asp	gtg Val	cca Pro 220	gat Asp	tat Tyr	gcg Ala	agc Ser	672
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr 25

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile 40

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`Ile	Tyr 50	Gly	Ala	Ser	Ser	Arg 55	Ala	Thr	Gly	Ile	Pro 60	Asp	Arg	Phe	Ser	
						gac Asp										240
						tat Tyr										288
						gly aaa										336
_	_			_		atc Ile		_			_		_	_		384
			_		_	gtg Val 135	_	_	_						_	432
	_		_	_		agg Arg		_		-			_			480
						gag Glu										528
	_	_		_	_	ctg Leu	_		_	_						576
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gcg Ala 225	-															678
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23

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
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Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro 85 90 95

Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys 115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg 130 135 140

Glu Ala Lys Val Gln Trp Arg Val Asp Asn Ala Leu Gln Ser Gly Asn 145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser 165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys 180 185 190

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<213> Homo sapiens

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<223> M1-25L

<400> 52

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Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asn Arg Phe Ser 50 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Phe 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr 180 185

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser 195 200 205

Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Asn 210 215 220

<210> 53

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<212> DNA

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				Ser					Glu					Tyr	tat Tyr	96
ggc	atg Met	cac His 35	tgg Trp	gtc Val	cgc Arg	cag Gln	gtt Val 40	cca Pro	ggc Gly	aag Lys	gly aaa	ctg Leu 45	gag Glu	tgg Trp	gtg Val	144
gca Ala	gct Ala 50	Val	tgg Trp	tat Tyr	gat Asp	gaa Glu 55	Ser	act Thr	aca Thr	tat Tyr	tct Ser 60	cca Pro	gac Asp	tcc Ser	gtg Val	192
aag Lys 65	ggc	cga Arg	ttc Phe	acc Thr	atc Ile 70	tcc Ser	aga Arg	gac Asp	gat Asp	tcc Ser 75	aag Lys	aac Asn	acg Thr	ctg Leu	tat Tyr 80	240
ctg Leu	caa Gln	atg Met	aac Asn	agc Ser 85	ctg Leu	aga Arg	gcc Ala	gag Glu	gac Asp 90	acg Thr	gct Ala	gtg Val	tat Tyr	tac Tyr 95	tgt Cys	288
gcg Ala	aga Arg	gat Asp	agg Arg 100	gtg Val	ggc Gly	ctc Leu	ttt Phe	gac Asp 105	tac Tyr	tgg Trp	ggc Gly	cag Gln	gga Gly 110	acc Thr	ctg Leu	336
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ctg Leu 145	gtc Val	aag Lys	gac Asp	tac Tyr	ttc Phe 150	ccc Pro	gaa Glu	ccg Pro	gtg Val	acg Thr 155	gtg Val	tcg Ser	tgg Trp	aac Asn	tca Ser 160	480
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ttg Leu	ggc Gly	acc Thr 195	cag Gln	acc Thr	tac Tyr	atc Ile	tgc Cys 200	aac Asn	gtg Val	aat Asn	cac His	aag Lys 205	ccc Pro	agc Ser	aac Asn	624

acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His 215 cac 675 His 225 <210> 54 <211> 225 <212> PRT <213> Homo sapiens <223> M1-1H <400> 54 Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Lys 10 Ser Leu Arg Leu Ser Cys Ala Ala Ser Glu Phe Thr Ile Ser Tyr Tyr 25 Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val 40 Ala Ala Val Trp Tyr Asp Glu Ser Thr Thr Tyr Ser Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 90 Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu 105 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu 120 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys 140 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser 155 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser 170 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser 185 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn 200 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His

His

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			Val		aag Lys			Glu								671
	cac His 225															677
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Lys 65	Gly	Arg	Phe	Thr	Ile 70	Ser	Arg	Asp	Asn	Ser 75	Lys	Asn	Thr	Leu	Tyr 80	
Leu	Gln	Met	Asn	Ser 85	Leu	Arg	Ala	Glu	Asp 90	Thr	Ala	Val	Tyr	Tyr 95	Cys	
Ala	Arg	Asp	Gly 100	Ile	Gly	Tyr	Phe	Asp 105	Tyr	Trp	Gly	Gln	Gly 110	Thr	Leu	
Val	Thr	Val 115	Ser	Ser	Ala	Ser	Thr 120	Lys	Gly	Pro	Ser	Val 125	Phe	Pro	Leu	
Ala	Pro 130	Ser	Ser	Lys	Ser	Thr 135	Ser	Gly	Gly	Thr	Ala 140	Ala	Leu	Gly	Cys	
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Gly	Ala	Leu	Thr	Ser 165	Gly	Val	His	Thr	Phe 170	Pro	Ala	Val	Leu	Gln 175	Ser	
Ser	Gly	Leu	Tyr 180	Ser	Leu	Ser	Ser	Val 185	Val	Thr	Val	Pro	Ser 190	Ser	Ser	
Leu	Gly	Thr 195	Gln	Thr	Tyr	Ile	Cys 200	Asn	Val	Asn	His	Lys 205	Pro	Ser	Asn	

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His 225

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		aag Lys														480
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192

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Ala Ala Val Trp Tyr Asp Gly Ser Thr Thr Tyr Ser Pro Asp Ser Val 55 Lys Gly Arg Phe Thr Ile Ser Arg Asp Ser Lys Asn Thr Leu Tyr 70 75 Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu 100 105 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu 120 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys 135 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser 150 155 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser 165 170 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser 185 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn 200 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His 215 220 His 225 <210> 67 <211> 675 <212> DNA <213> Homo sapiens <220> <223> M1-23H <220> <221> CDS <222> (1)..(675) cag gtg cag ctg gtg cag tct ggg gga ggc gtg gtc cag cct ggg agg 48 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg tcc ctg aga ctc tcc tgt gca gcg tct gga ttc acc ttc agt aac tat 96 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144

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8

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61 ⁷ 336	ato Met	g cad His	3 Trp	gto Val	cgc Arg	cag Gln	gtt Val 40	. Pro	ggc Gly	aag Lys	g gly	ctg Leu 45	Glu	j tg <u>ç</u> ı Trp	g gtg Val	144
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35 40

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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95

Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu 115 120 125

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Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn 195 200 205

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atc Ile	tat Tyr 50	ggt Gly	gca Ala	tcc Ser	agc Ser	agg Arg 55	gcc Ala	act Thr	ggc Gly	atc Ile	cca Pro 60	gac Asp	agg Arg	ttc Phe	agt Ser	192
ggc Gly 65	agt Ser	gly aaa	tct Ser	Gly ggg	aca Thr 70	gac Asp	ttc Phe	act Thr	ctc Leu	acc Thr 75	atc Ile	agc Ser	aga Arg	ctg Leu	gag Glu 80	240
cct Pro	gaa Glu	gat Asp	ttt Phe	gca Ala 85	gtg Val	tat Tyr	tac Tyr	tgt Cys	cag Gln 90	cag Gln	tat Tyr	ggt Gly	agc Ser	tca Ser 95	cct Pro	288
cca Pro	ttc Phe	act Thr	ttc Phe 100	ggc Gly	cct Pro	Gly aaa	acc Thr	aaa Lys 105	gtg Val	gat Asp	atc Ile	aaa Lys	cga Arg 110	act Thr	gtg Val	336
gct Ala	gca Ala	cca Pro 115	tct Ser	gtc Val	ttc Phe	atc Ile	ttc Phe 120	ccg Pro	cca Pro	tct Ser	gat Asp	gag Glu 125	cag Gln	ttg Leu	aga Arg	384
tct Ser	gga Gly 130	act Thr	gcc Ala	tct Ser	gtt Val	gtg Val 135	tgc Cys	ctg Leu	ctg Leu	aat Asn	aac Asn 140	ttc Phe	tat Tyr	ccc Pro	aga Arg	432
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ctc Leu	agc Ser	agc Ser	acc Thr 180	ctg Leu	acg Thr	ctg Leu	agc Ser	aaa Lys 185	gca Ala	gac Asp	tac Tyr	gag Glu	aaa Lys 190	cac His	aaa Lys	576
gtc Val	tac Tyr	gcc Ala 195	tgc Cys	gaa Glu	gtc Val	acc Thr	cat His 200	cag Gln	ggc Gly	ctg Leu	agc Ser	tcg Ser 205	ccc Pro	gtc Val	aca Thr	624
aag Lys	agc Ser 210	ttc Phe	aac Asn	agg Arg	gga Gly	gag Glu 215	tct Ser	tat Tyr	cca Pro	tat Tyr	gat Asp 220	gtg Val	cca Pro	gat Asp	tat Tyr	672
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Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu 35 40

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro 85 90 95

Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Arg 115 120 125

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg 130 135 140

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn 145 150 155 160

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser 165 170 175

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
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Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr 195 200 205

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tac Tyr																144
atc Ile																192
ggc Gly 65																240
cct Pro																288
ccg Pro																336
gct (384
tct Ser																432
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tcc Ser																528
ctc Leu	agc Ser	agc Ser	acc Thr 180	ctg Leu	acg Thr	ctg Leu	agc Ser	aaa Lys 185	gca Ala	gac Asp	tac Tyr	gag Glu	aaa Lys 190	cac His	aaa Lys	576
gtc Val	tac Tyr	gcc Ala 195	tgc Cys	gaa Glu	gtc Val	acc Thr	cat His 200	cag Gln	ggc Gly	ctg Leu	agc Ser	tcg Ser 205	ccc Pro	gtc Val	aca Thr	624

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			ctc acc atc Leu Thr Ile 75		
		-	cag cag tat Gln Gln Tyr 90		
Thr Phe Gly I			atc aaa cga Ile Lys Arg		
			gat gag cag Asp Glu Gln		
			aac ttc tat Asn Phe Tyr 140		
			ctc caa tcg Leu Gln Ser 155		
			gac agc acc Asp Ser Thr 170		
_			tac gag aaa Tyr Glu Lys	_	

180 185 190

gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc 624
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

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Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser 50 55 60

Val Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Phe 85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr 180 185 190

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tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu 35 40 45	ctc 144 Leu
atc tat ggt gca tcc agc agg gcc act ggc atc cca gac agg ttc Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe 50 55 60	agt 192 Ser
ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu 65 70 75	gag 240 Glu 80
cct gaa gat ttt gca gtg tat tac tgt cag cag tat gtt agc tca Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Ser Ser 85 90 95	
act ttc ggc cct ggg acc aaa gtg gat atc aaa cga act gtg gct Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala 100 105 110	gca 336 Ala
cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser 115 120 125	
act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu 130 135 140	
aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser 145 150 155	cag 480 Gln 160
gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu 165 170 175	agc 528 Ser
agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val 180 185 190	tac 576 Tyr

672

gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser 200 ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser 215 220 <210> 78 <211> 224 <212> PRT <213> Homo sapiens <223> M2-18L <400> 78 Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Val Ser Ser Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln 145 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser 215 210

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tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu 35 40 45	:
atc tac ggt gca tcc agg agg gcc act ggc atc cca gac agg ttc agt Ile Tyr Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser 50 55 60	1
ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu 65 70 75 80	1
cct gaa gat ttt gca gtg tat tac tgt cag cag tat ggt agc tca ccc 288 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro 85 90 95	ı
atg tac act ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg 336 Met Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val 100 105 110	ï
gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa 384 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys 115 120 125	:
tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga 432 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg 130 135 140	:
gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac 480 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn 145 150 155 160)
tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc 528 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser 165 170 175	3
ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 576 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys 180 185 190	5

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aag Lys	agc Ser 210	ttc Phe	aac Asn	agg Arg	gga Gly	gag Glu 215	tct Ser	tat Tyr	cca Pro	tat Tyr	gat Asp 220	gtg Val	cca Pro	gat Asp	tat Tyr	672
gcg Ala 225	_															678
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Tyr	Leu	Ala 35	Trp	Tyr	Gln	Gln	Lys 40	Pro	Gly	Gln	Ala	Pro 45	Arg	Leu	Leu	
Ile	Tyr 50	Gly	Ala	Ser	Arg	Arg 55	Ala	Thr	Gly	Ile	Pro 60	Asp	Arg	Phe	Ser	
Gly 65	Ser	Gly	Ser	Gly	Thr 70	Asp	Phe	Thr	Leu	Thr 75	Ile	Ser	Arg	Leu	Glu 80	
Pro	Glu	Asp	Phe	Ala 85	Val	Tyr	Tyr	Cys	Gln 90	Gln	Tyr	Gly	Ser	Ser 95	Pro	
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Glu 145	Ala	Lys	Val	Gln	Trp 150	Lys	Val	Asp	Asn	Ala 155	Leu	Gln	Ser	Gly	Asn 160	
Ser	Gln	Glu	Ser	Val 165	Thr	Glu	Gln	Asp	Ser 170	Lys	Asp	Ser	Thr	Tyr 175	Ser	
Leu	Ser	Ser	Thr 180	Leu	Thr	Leu	Ser	Lys 185	Ala	Asp	Tyr	Glu	Lys 190	His	Lys	
Val	Tyr	Ala 195	Cys	Glu	Val	Thr	His 200	Gln	Gly	Leu	Ser	Ser 205	Pro	Val	Thr	
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165 170 175

age ace etg acg etg age aaa gea gae tae gag aaa eae aaa gte tae 576 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr 180 gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc 624 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser 195 200 ttc aac agg gga gag tct tat cca tat gat gtg cca gat tat gcg agc 672 Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser 215 <210> 82 <211> 224 <212> PRT <213> Homo sapiens <223> M2-31L <400> 82 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly 10 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr 25 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile 40 Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Thr Asn Trp Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala 105 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly 120 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln 155 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser

Phe Asn Arg Gly Glu Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser 210 215 220

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													ctc Leu			144
													ttc Phe			192
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													tgg Trp			288
													gtg Val 110			336
cca Pro	tct Ser	gtc Val 115	ttc Phe	atc Ile	ttc Phe	ccg Pro	cca Pro 120	tct Ser	gat Asp	gag Glu	cag Gln	ttg Leu 125	aaa Lys	tct Ser	gga Gly	384
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aaa Lys 145	gta Val	cag Gln	tgg Trp	aag Lys	gtg Val 150	gat Asp	aac Asn	gcc Ala	ctc Leu	caa Gln 155	tcg Ser	ggt Gly	aac Asn	tcc Ser	cag Gln 160	480
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Leu	Ala	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Gln	Ala	Pro	Arg 45	Leu	Leu	Ile	
Tyr	Asp 50	Ala	Ser	Asn	Arg	Ala 55	Ala	Gly	Ile	Pro	Ala 60	Arg	Phe	Ser	Gly	
Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Leu	Thr	Ile 75	Ser	Ser	Leu	Glu	Pro 80	
Glu	Asp	Phe	Ala	Val 85	Tyr	Tyr	Cys	Gln	Gln 90	Arg	Asn	Asn	Trp	Pro 95	Leu	
Thr	Phe	Gly	Gly 100	Gly	Thr	Lys	Val	Glu 105	Ile	Lys	Arg	Thr	Val 110	Ala	Ala	
Pro	Ser	Val 115	Phe	Ile	Phe	Pro	Pro 120	Ser	Asp	Glu	Gln	Leu 125	Lys	Ser	Gly	
Thr	Ala 130	Ser	Val	Val	Cys	Leu 135	Leu	Asn	Asn	Phe	Tyr 140	Pro	Arg	Glu	Ala	
Lys 145	Val	Gln	Trp	Lys	Val 150	Asp	Asn	Ala	Leu	Gln 155	Ser	Gly	Asn	Ser	Gln 160	
Glu	Ser	Val	Thr	Glu 165	Gln	Asp	Ser	Lys	Asp 170	Ser	Thr	Tyr	Ser	Leu 175	Ser	
Ser	Thr	Leu	Thr 180	Leu	Ser	Lys	Ala	Asp 185	Tyr	Glu	Lys	His	Lys 190	Val	Tyr	
Ala	Cys	Glu 195	Val	Thr	His	Gln	Gly 200	Leu	Ser	Ser	Pro	Val 205	Thr	Lys	Ser	
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Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
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Gly	Ala	Leu	Thr	Ser 165	Gly	Val	His	Thr	Phe 170	Pro	Ala	Val	Leu	Gln 175	Ser	

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130

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser 150 145 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser 170 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser 185 180 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Ser 200 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His 215 210 His 225 <210> 95 <211> 675 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(675) <220> <223> M2-16H <400> 95 cag gtg cag ctg gtg cag tct ggg gga ggc gtg gtc cag cct ggg aag 48 Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Lys tcc ctg aga ctc tcc tgt gca gcg tct gga ttc agc ttg agt tac tat 96 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Ser Tyr Tyr 20 ggc atg cac tgg gtc cgc cag gtt cca ggc aag ggg ctg gag tgg gtg 144 Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val 40 35 gca gct gtc tgg tat gat gga agt act aga tat tct cca gac tcc gtg 192 Ala Ala Val Trp Tyr Asp Gly Ser Thr Arg Tyr Ser Pro Asp Ser Val 50 aag ggc cga ttc acc atc tcc aga gac gat tcc aag aac acg ctg tat 240 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr 65 70 ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 gcg aga gat agg gtg ggc ctc ttt gac tac tgg ggc cag gga acc ctg 336 Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu 105 100

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Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu 115 120 125 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys 135 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser 150 155 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser 170 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser 180 185 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn 200 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His 215 His 225 <210> 97 <211> 675 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(675) <220> <223> M2-18H <400> 97 cag gtg cag ctg gtg cag tct ggg gga ggc gtg gtc cag cct ggg aag Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Lys tee etg aga ete tee tgt gea geg tet gga tte age tte agt tae tat 96 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Tyr Tyr ggc atg cac tgg gtc cgc cag gtt cca ggc aag ggg ctg gag tgg gtg 144 Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val gca gct gtc tgg tat gat gga agt act aca tat tct cca gac tcc gtg 192 Ala Ala Val Trp Tyr Asp Gly Ser Thr Thr Tyr Ser Pro Asp Ser Val aag ggc cga ttc acc atc tcc aga gac gat tcc aag aac acg ctg tat Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr 65 ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

95 90 85 gcg aga gat agg gtg ggc ctc ttt gac tac tgg ggc cag gga acc ctg Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu 100 105 gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu 115 120 gea eee tee tee aag age ace tet ggg gge aca geg gee etg gge tge Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys 135 ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca 480 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser 170 tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser 185 ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn 200 acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His 215 220 675 cac His 225 <210> 98 <211> 225 <212> PRT <213> Homo sapiens <223> M2-18H <400> 98 Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Lys Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Tyr Tyr Gly Met His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val Ala Ala Val Trp Tyr Asp Gly Ser Thr Thr Tyr Ser Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Ser Lys Asn Thr Leu Tyr 75

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 Ala Arg Asp Arg Val Gly Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu 105 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu 120 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser 150 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser 170 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn 200 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His 210 215 His 225 <210> 99 <211> 675 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(675) <220> <223> M2-20H <400> 99 cag gtg cag ctg gtg cag tct ggg gga ggc gtg gtc cag cct ggg agg Gln Val Gln Leu Val Gln Ser Gly Gly Val Val Gln Pro Gly Arg tee etg agg ete tee tgt gea gee tet gga tte aet tte agt tae tat Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr 20 ggt atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 tca ctt ata aca tat gat gga agg aat aaa tac tac gcc gac tcc gtg Ser Leu Ile Thr Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val 55 50

														ctg Leu		240
														tac Tyr 95		288
_	_	_						_				_		atc Ile	_	336
_		-			_			_			_	_		ccc Pro	_	384
														ggc Gly		432
														aag Lys		480
	_	_		_						_	_	_		cag Gln 175		528
						_	_							agc Ser	_	576
														agc Ser		624
														cac His		672
cac His 225																675
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	> 10 Val		Leu	Val 5	Gln	Ser	Gly	Gly	Gly 10	Val	Val	Gln	Pro	Gly 15	Arg	
Ser	Leu	Arg	Leu 20	Ser	Cys	Ala	Ala	Ser 25	Gly	Phe	Thr	Phe	Ser 30	Tyr	Tyr	
Gly	Met	His 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45	Glu	Trp	Val	

Ser Leu Ile Thr Tyr Asp Gly Arg Asn Lys Tyr Tyr Ala Asp Ser Val 55 Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ser Lys Asn Thr Leu Tyr 70 Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Glu Tyr Tyr Cys 90 Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Ile Leu 105 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Lys Ser 150 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser 170 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn 200 Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His His 215 His 225 <210> 101 <211> 675 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(675) <220> <223> M2-31H <400> 101 cag gtg cag ctg gtg gag tct ggg gga gtc gtg gtc cag cct ggg agg Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acg ttc agt tac tat Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr 20 ggt ata cac tgg gtc cgc cag gtt cca ggc aag gga cta gag tgg gtg Gly Ile His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val

45 35 40 gca ctt ata tca tac gat gga agc aat aaa tac tac gca gac tcc gtg Ala Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac act ctg tat Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 ctg caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys gcg aga gac tgg atc ggg tac ttt gac tac tgg ggc cag gga acc ctg 336 Ala Arg Asp Trp Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu 100 gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu 115 120 gca eec tee tee aag age ace tet ggg gge aca geg gee etg gge tge 432 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys 130 135 ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser 150 ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc 576 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser 180 185 ctg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac 624 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn 200 acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His 675 cac His 225 <210> 102 <211> 225 <212> PRT <213> Homo sapiens <223> M2-31H <400> 102 Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr 20 25 30

Gly Ile His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ala Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val 50 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys 130 135

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His 210 220

His 225

<210> 103

<211> 708

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(708)

<220>

<223> M2-32H

<400> 103

cag gtg cag ctg gtg cag tct ggg gga ggc ttg gta cat cct ggg ggg
Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly
1 5 10 15

		aga Arg											96
		cac His 35		_	_	_	_			_	 	_	144
		agt Ser											192
		ttc Phe											240
		aac Asn											288
		tat Tyr											336
		atg Met 115	Asp										384
_		acc Thr	_			_	_						432
		tct Ser											480
		gaa Glu	_		_		_						528
		cac His											576
		agc Ser 195											624
		tgc Cys											672
	_	gag Glu											708

<210> 104

<211> 236 <212> PRT

<213> Homo sapiens

<223> M2-32H

<400> 104

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val His Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Gly Ser Gly Phe Ile Phe Arg Asn His 20 25 30

Pro Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ser Val Ser Gly Ile Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val Lys
50 60

Gly Arg Phe Ser Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys Ala 85 90 95

Arg Glu Tyr Tyr Tyr Gly Ser Gly Ser Tyr Arg Val Asp Tyr Tyr Tyr 100 105 110

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys 130 135 140

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr 145 150 155 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser 165 170 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser 180 185 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr 195 200 205

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys 210 215 220

Lys Ala Glu Pro Lys Ser His His His His His 225 230 235

<210> 105

<211> 675

<212> DNA

<213> Homo sapiens

<220>

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tcc Ser	ctg Leu	aga Arg	ctc Leu 20	tcc Ser	tgt Cys	gca Ala	gcg Ala	tct Ser 25	gga Gly	ttt Phe	acc Thr	ttc Phe	agt Ser 30	tac Tyr	tat Tyr	96
ggc	atg Met	cac His 35	tgg Trp	gtc Val	cgc Arg	cag Gln	gct Ala 40	cca Pro	ggc Gly	aag Lys	Gly aaa	ctg Leu 45	gaa Glu	tgg Trp	atg Met	144
									aaa Lys							192
		_					_	_	aat Asn		_		_	_		240
									gac Asp 90							288
									tat Tyr							336
									ggc Gly							384
									ggc Gly							432
									gtg Val							480
									ttc Phe 170							528
									gtg Val							576
ttg Leu	ggc Gly	acc Thr 195	cag Gln	acc Thr	tac Tyr	atc Ile	tgc Cys 200	aac Asn	gtg Val	aat Asn	cac His	aag Lys 205	ccc Pro	agc Ser	aac Asn	624
									aaa Lys							672
cac His 225																675

<210> 106

<211> 225

<212> PRT

<213> Homo sapiens

<223> M2-33H

<400> 106

Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met 35 40 45

Thr Leu Ile Thr Tyr Asp Gly Asp Asn Lys Tyr Tyr Ala Asp Ser Val 50 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His 210 215 220

His 225

<210> 107

<211> 675

<212> DNA

<213> Homo sapiens

<221> CDS <222> (1)..(675) <220> <223> M2-34H <400> 107 cag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag cct ggg agg 48 Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acg ttc agt tac tat 96 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr ggt ata cac tgg gtc cgc cag gtt cca ggc aag gga cta gag tgg gtg 144 Gly Ile His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val gta ctt ata tca tac gat gga agc aat aaa tac tac gca gac tcc gtg 192 Val Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac act ctg tat 240 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 ctg caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tqt 288 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys gcg aga gac tgg atc ggg tac ttt gac tac tgg ggc cag gga acc ctg 336 Ala Arg Asp Trp Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu 100 gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg 384 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu 115 gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tqc 432 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys 130 ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca 480 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc 528 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser tea gga etc tac tee etc age age gtg gtg ace gtg ecc tee age age 576 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser 180 ctg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac 624 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn 200 acc aag gtg gac aag aaa gca gag ccc aaa tct cat cac cat cac cat

.

<220>

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His Essential 210 215 220

cac His 225 675

<210> 108

<211> 225

<212> PRT

<213> Homo sapiens

<223> M2-34H

<400> 108

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Tyr
20 25 30

Gly Ile His Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
35 40

Val Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val 50 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Trp Ile Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn 195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser His His His His Essential 210 215 220

His

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<220> <221> CDS <222> (1)(0															
<220> <223> M2-35H															
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tcc ctg aga	ctc tcc tgt Leu Ser Cys 20	gca gcc tct Ala Ala Ser 25	gga ttc acg Gly Phe Thr	atc agt tac Ile Ser Tyr 30	tat 96 Tyr										
ggt ata cac Gly Ile His 35	tgg gtc cgc Trp Val Arg	cag gtt cca Gln Val Pro 40	ggc aag gga Gly Lys Gly	cta gag tgg Leu Glu Trp 45	gtg 144 Val										
gaa ctt ata Glu Leu Ile 50	tca tac gat Ser Tyr Asp	gga agc aat Gly Ser Asn 55	aaa tac tac Lys Tyr Tyr 60	gca gac tcc Ala Asp Ser	gtg 192 Val										
aag ggc cga Lys Gly Arg 65	ttc acc atc Phe Thr Ile 70	tcc aga gac Ser Arg Asp	aat tcc aag Asn Ser Lys 75	aac act ctg Asn Thr Leu	tat 240 Tyr 80										
ctg caa atg Leu Gln Met	aac agc ctg Asn Ser Leu 85	aga gct gag Arg Ala Glu	gac acg gct Asp Thr Ala 90	gtg tat tac Val Tyr Tyr 95	tgt 288 Cys										
gcg aga gac Ala Arg Asp	tgg atc ggg Trp Ile Gly 100	tac ttt gac Tyr Phe Asp 105	tac tgg ggc Tyr Trp Gly	cag gga acc Gln Gly Thr 110	ctg 336 Leu										
gtc acc gtc Val Thr Val 115	tcc tca gcc Ser Ser Ala	tcc acc aag Ser Thr Lys 120	ggc cca tcg Gly Pro Ser	gtc ttc ccc Val Phe Pro 125	ctg 384 Leu										
gca ccc tcc Ala Pro Ser 130	tcc aag agc Ser Lys Ser	acc tct ggg Thr Ser Gly 135	ggc aca gcg Gly Thr Ala 140	gcc ctg ggc Ala Leu Gly	tgc 432 Cys										
ctg gtc aag Leu Val Lys 145	gac tac ttc Asp Tyr Phe 150	Pro Glu Pro	gtg acg gtg Val Thr Val 155	tcg tgg aac Ser Trp Asn	tca 480 Ser 160										
ggc gcc ctg Gly Ala Leu	acc agc ggc Thr Ser Gly 165	gtg cac acc Val His Thr	ttc ccg gct Phe Pro Ala 170	gtc cta cag Val Leu Gln 175	ser										
tca gga ctc Ser Gly Leu	tac tcc ctc Tyr Ser Leu 180	agc agc gtg Ser Ser Val 185	gtg acc gtg Val Thr Val	ccc tcc ago Pro Ser Ser 190	agc 576 Ser										

ctg Leu	ggc Gly	acc Thr 195	cag Gln	acc Thr	tac Tyr	Ile	tgc Cys 200	aac Asn	gtg Val	aat Asn	cac His	aag Lys 205	ccc Pro	agc Ser	aac Asn
acc Thr	aag Lys 210	gtg Val	gac Asp	aag Lys	aaa Lys	gca Ala 215	gag Glu	ccc Pro	aaa Lys	tct Ser	cat His 220	cac His	cat His	cac His	cat His
cac His 225															
<213 <213 <213	<210> 110 <211> 225 <212> PRT <213> Homo sapiens <223> M2-35H														
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Ser	Leu	Arg	Leu 20	Ser	Cys	Ala	Ala	Ser 25	Gly	Phe	Thr	Ile	Ser 30	Tyr	Tyr
Gly	Ile	His 35	Trp	Val	Arg	Gln	Val 40	Pro	Gly	Lys	Gly	Leu 45	Glu	Trp	Val
Glu	Leu 50	Ile	Ser	Tyr	Asp	Gly 55	Ser	Asn	Lys	Tyr	Tyr 60	Ala	Asp	Ser	Val
Lys 65	Gly	Arg	Phe	Thr	Ile 70	Ser	Arg	Asp	Asn	Ser 75	Lys	Asn	Thr	Leu	Tyr 80
Leu	Gln	Met	Asn	Ser 85	Leu	Arg	Ala	Glu	Asp 90	Thr	Ala	Val	Tyr	Tyr 95	Cys
Ala	Arg	Asp	Trp		Gly	Tyr	Phe	Asp 105	туг	Trp	Gly	Gln	Gly 110	Thr	Leu
Val	Thr	Val 115		Ser	Ala	Ser	Thr 120	Lys	Gly	Pro	Ser	Val 125	Phe	Pro	Leu
Ala	Pro 130		Ser	Lys	Ser	Thr 135	Ser	Gly	Gly	Thr	Ala 140	Ala	Leu	Gly	Cys
Leu 145		Lys	Asp	Tyr	Phe 150	Pro	Glu	Pro	Val	. Thr 155	Val	Ser	Trp	Asn	Ser 160
Gly	Ala	Leu	Thr	Ser 165	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln 175	Ser
Ser	Gly	Leu	туг 180		Leu	Ser	Ser	Val 185	. Val	Thr	Val	Pro	Ser 190	Ser	Ser
Leu	Gly	Thr 195		Thr	Tyr	Ile	Cys		ı Val	l Asn	His	205	Pro	Ser	Asn
Thr	Lys	val	Asp	Lys	Lys	Ala	Glu	Pro	Lys	s Ser	His	His	: His	His	His

220 215 210

His 225

<210> 111

<211> 70

<212> DNA <213> Artificial Sequence

<223> Description of Artificial Sequence: Figure 2 Kappa Chain

<400> 111

tatttccagc ttggtccctc tagagttaac gatatcaacg tttatctaat cagcaagaga 60 tggaggcttg

<210> 112

<211> 70

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Figure 2 Heavy Chain

<400> 112

tgaggttcct tgaccccact gcagagtact aggcctctga gctactcagt taggtgattg 60 agtagccagt